



PCT10

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/088,920

DATE: 10/23/2002  
 TIME: 16:11:55

*Error on p. 4*

Input Set : A:\25835104.app  
 Output Set : N:\CRF4\10232002\J088920.raw

3 <110> APPLICANT: KIZAKI, NORIYUKI  
 4 YASOHARA, YOSHIHIKO  
 5 HASEGAWA, JUNZO  
 7 <120> TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING  
 THE SAME

9 <130> FILE REFERENCE: 025835/0104  
 11 <140> CURRENT APPLICATION NUMBER: 10/088,920  
 12 <141> CURRENT FILING DATE: 2002-06-03  
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06619  
 15 <151> PRIOR FILING DATE: 2001-08-01  
 17 <150> PRIOR APPLICATION NUMBER: JP 2000-232756  
 18 <151> PRIOR FILING DATE: 2000-08-01  
 20 <160> NUMBER OF SEQ ID NOS: 11

21 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 277

24 <212> TYPE: PRT

25 <213> ORGANISM: Micrococcus luteus

27 <400> SEQUENCE: 1

28 Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly	
29 1 5 10 15	
31 Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu	
32 20 25 30	
34 Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp	
35 35 40 45	
37 Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu	
38 50 55 60	
40 Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met	
41 65 70 75 80	
43 Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser	
44 85 90 95	
46 Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp	
47 100 105 110	
49 Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu	
50 115 120 125	
52 Val Ile Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His	
53 130 135 140	
55 Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr	
56 145 150 155 160	
58 Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp	
59 165 170 175	
61 Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser	
62 180 185 190	
64 Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val	
65 195 200 205	

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```

67 Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val
68      210      215      220
70 Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln
71 225      230      235      240
73 His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu
74      245      250      255
76 Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg
77      260      265      270
79 Pro Leu Glu Met Leu
80      275
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 1410
85 <212> TYPE: DNA
86 <213> ORGANISM: Micrococcus luteus
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (108)..(938)
92 <400> SEQUENCE: 2
93 ggtaccggcc gccctcctat aagccagcac cggtcgagga cgcgcgggcc cttegaggat 60
95 ctcaqccac gtcgcgcctc aggacaacca gaaggaagtg atcgcg atg cga cgg 116
96                                     Met Arg Arg
97                                     1
98 atg acg ctg ccg aat ggg ggg tcc atc cct gta ctg ggc cag ggc acc 164
100 Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly Gln Gly Thr
101      5      10      15
103 tgg ggc tgg ggt gag gac ccc ggc cgc cgc ggc gac gag gtc gcc ggc 212
104 Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu Val Ala Ala
105 20      25      30      35
107 ctg cac gcc ggc ctc gag ctg ggc atg acg ctg gtc gac acc gcc gag 260
108 Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp Thr Ala Glu
109      40      45      50
111 atg tac gcc gac ggc ggt ggc gag gag gtc gct ggt gaa gca ttg ggc 308
112 Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu Ala Leu Ala
113      55      60      65
115 ggt cgc cgc gac gac ggc ttc gtc gtc agc aag gtc atg ccg tcc cac 356
116 Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met Pro Ser His
117      70      75      80
119 gcc tcc cgt tcc ggc acc atc ggc gcc tgc gaa cgc agc ctg aaa cgc 404
120 Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser Leu Lys Arg
121      85      90      95
123 ctc ggc acc gat ccg atc gac ctc tac ctg ctg gac tcc cac ggc agc 452
124 Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp Gln Gly Arg
125 100      105      110      115
127 tcc ccg cag cag gac acc gtc ggc gcc ttc cgc cag ctc gcc gac gac 500
128 Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu Val Gln Asp
129      120      125      130
131 ggc aaa atc cga tac tgg ggc gtc agc aac ttc gac cac ccg ggc ctc 548
132 Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His Arg Ala Leu
133      135      140      145

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```

135 gcc gag ctg cag gac ctg ccg gcc acc agc ggg ctg acc acg gat cag 596
136 Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr Thr Asp Gln
137      150      155      160
139 gtg ctg tac aac ctg tcg cgg cga gga ccg gag tac gac ctg ctg ccg 644
140 Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp Leu Leu Pro
141      165      170      175
143 tgg tgc gcc gac cac cag ctg ccg gtc atg gcg tac tcg ccg atc gag 692
144 Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser Pro Ile Glu
145 180      185      190      195
147 cag gcc cgc atc ctt gac gac acg acg ctg aac gac gtc gcg gcc cgt 740
148 Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val Ala Ala Arg
149      200      205      210
151 cac agc gtc agc ccc gcg gcg gcg gcc ctt gcc tgg gtg ctg cgc cgc 788
152 His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val Leu Arg Arg
153      215      220      225
155 gac tcg ctc tgc acg atc ccc aag gcg agc agc ccg cag cac gtg cgc 836
156 Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln His Val Arg
157      230      235      240
159 gac aac gcc aca gca ctg gac gtg gag ctg acc cgc gaa gac ctg gat 884
160 Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu Asp Leu Asp
161      245      250      255
163 gct ctg gac cgt gcg ttt ccg ccc ccg agc gga ccg cga cca ctg gaa 932
164 Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg Pro Leu Gln
165 260      265      270      275
167 atg ctg tgacctgcc ccagggcgca gccgggtcgg tcggggcggt ccgggcagtc 988
168 Met Leu
170 cgggcagcgc tcgggtcagc gcaagtctcc gaaggacctg cctgtcacct cctcctgaac 1048
172 ctgtgcacgc catccatcga ctctttcct cgagccctgt cgggttcgcg gtaggcgctg 1108
174 atcatccgct ggcaggtccc ccaagtggcc tcgagccggg cctctgctt gtcggtgagc 1168
176 aaccgggttc cgcgtgcag ggttcgacgg gcggagtga ggggttcgc cgtgcggccg 1228
178 cagtgccat gcaggtcctg ctggaccgg cgggtggcag ggaccaacgc gtcgcggct 1288
180 aaccggaact cgagcgactg gcgttggtga cgcagacgac ctggacactg ggcgtgcgg 1348
182 tcaggaggat ctccaaagtc ggcgggcggg gttcaggcga tgtcaggaa ggaacggagc 1408
184 tc 1410
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 20
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
195 <220> FEATURE:
196 <221> NAME/KEY: modified_base
197 <222> LOCATION: (6)
198 <223> OTHER INFORMATION: a, t, c, g, other or unknown
200 <220> FEATURE:
201 <221> NAME/KEY: modified_base
202 <222> LOCATION: (9)
203 <223> OTHER INFORMATION: a, t, c, g, other or unknown
205 <400> SEQUENCE: 3

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Input Set : A:\25835104.app

Output Set: N:\CRF4\10232002\J088920.raw

W--> 206 **gayaacngcng aratgtaygc** 20  
 209 <210> SEQ ID NO: 4  
 210 <211> LENGTH: 20  
 211 <212> TYPE: DNA  
 212 <213> ORGANISM: Artificial Sequence  
 214 <220> FEATURE:  
 215 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 217 <220> FEATURE:  
 218 <221> NAME/KEY: modified\_base  
 219 <222> LOCATION: (6)  
 220 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
 222 <220> FEATURE:  
 223 <221> NAME/KEY: modified\_base  
 224 <222> LOCATION: (6) *n found at position 9*  
 225 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
 227 <400> SEQUENCE: 4

W--> 228 **tcytcnacna gytgrtgraa** 20  
 231 <210> SEQ ID NO: 5  
 232 <211> LENGTH: 26  
 233 <212> TYPE: DNA  
 234 <213> ORGANISM: Artificial Sequence  
 236 <220> FEATURE:  
 237 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 239 <400> SEQUENCE: 5  
 240 ggcgaatgac gacggatgac gctgcc 26  
 243 <210> SEQ ID NO: 6  
 244 <211> LENGTH: 32  
 245 <212> TYPE: DNA  
 246 <213> ORGANISM: Artificial Sequence  
 248 <220> FEATURE:  
 249 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 251 <400> SEQUENCE: 6  
 252 ggcgaattct tacagcattt ccagtggtcg cg 32  
 255 <210> SEQ ID NO: 7  
 256 <211> LENGTH: 46  
 257 <212> TYPE: DNA  
 258 <213> ORGANISM: Artificial Sequence  
 260 <220> FEATURE:  
 261 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 263 <400> SEQUENCE: 7  
 264 ggcgaattcta aggagattta tatatgcgac ggaatgacct gccgac 46  
 267 <210> SEQ ID NO: 8  
 268 <211> LENGTH: 29  
 269 <212> TYPE: DNA  
 270 <213> ORGANISM: Artificial Sequence  
 272 <220> FEATURE:  
 273 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 275 <400> SEQUENCE: 8  
 276 caggagctct tacagcattt ccagtggtc 29

## RAW SEQUENCE LISTING

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Input Set : A:\25835104.app

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```

279 <210> SEQ ID NO: 9
280 <211> LENGTH: 144
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
286     double-stranded DNA
288 <400> SEQUENCE: 9
289 gaatttctaag gagatttaca tatgcgtcgt atgactttac catctggtga atctattcca      60
290 gtttttaggtc aaggtacttg gggttggggg gaagatccag gtcgtcgtgg tgatgaagtt      120
291 gctgcttttac atgtggtctc cgag                                           144
294 <210> SEQ ID NO: 10
295 <211> LENGTH: 33
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
302 <400> SEQUENCE: 10
303 caggagctct aaggaggta acaatgtata aag                                           33
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 28
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
314 <400> SEQUENCE: 11
315 caccgatact tatccgcgtc ctgcttgg                                           28

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/088,920

DATE: 10/23/2002  
TIME: 16:11:56

Input Set : A:\25835104.app  
Output Set: N:\CRF4\10232002\J088920.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,9  
Seq#:4; N Pos. 6,9

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/088,920

DATE: 10/23/2002

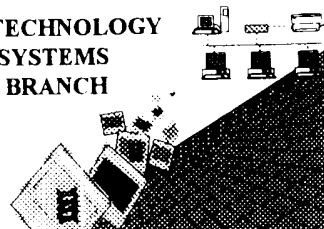
TIME: 16:11:56

Input Set : A:\25835104.app

Output Set: N:\CRF4\10232002\J088920.raw

L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0

L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0



hth

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/088,920  
Source: PC710  
Date Processed by STIC: 10/23/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
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Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202